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RPS-BLAST 2.2.6 [Apr-09-2003]

Query= local sequence:
(144 letters)

Database: #cdd.v1.62
11,088 PSSMs; 2,717,223 total columns

Click on boxes for multiple alignments



PSSMs producing significant alignments:		Score (bits)	E value
gnlCDDI5069	pfam03311, Cornichon, Cornichon protein	<u>142</u>	1e-35

[gnlCDDI5069](#), pfam03311, Cornichon, Cornichon protein.

CD-Length = 130 residues, 89.2% aligned
Score = 142 bits (360), Expect = 1e-35

Query: 6	AAFCYMLALLLTAALIFFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPPEYLIHAFFCVM	65
Sbjct: 1	AAFCFILTLILNCALIFFQIYFVIAYADLETDYINPIDQCRRLNRLVLPPEYGLHAFLCLL	60
Query: 66	FLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYVQKEGWCK	122
Sbjct: 61	FLLSGHWFMLLNPLLAYNIWRYMKRPVMSHP-LYDPTTIFNRDTLKSCQKESWIK	116

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results of **BLAST****BLASTP 2.2.6 [Apr-09-2003]****Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1055020477-012902-31232

Query=

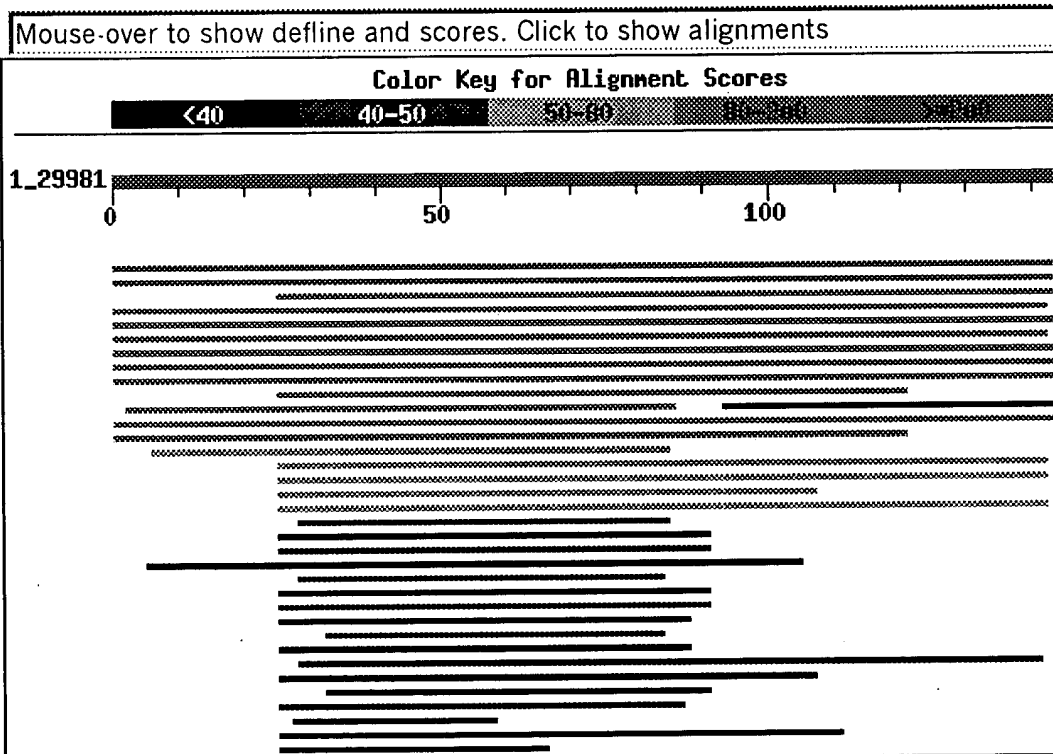
(144 letters)

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF

1,442,039 sequences; 463,592,631 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 36 Blast Hits on the Query Sequence




Sequences producing significant alignments:

	Score (bits)	E Value
--	-----------------	------------

gi 5031639 ref NP_005767.1	cornichon-like [Homo sapiens] >...	205	1e-52	<input checked="" type="checkbox"/>
gi 27545445 ref NP_034049.1	cornichon homolog [Mus musculu...	202	6e-52	<input checked="" type="checkbox"/>
gi 4894209 gb AAD32301.1	cornichon-like protein [Homo sapi...	191	2e-48	
gi 13195570 gb AAK15762.1 AF329820.1	cornichon [Boltenia vi...	164	2e-40	
gi 17137046 ref NP_477068.1	cornichon CG5855-PB [Drosophil...	151	2e-36	<input checked="" type="checkbox"/>
gi 6753470 ref NP_034050.1	cornichon-like [Mus musculus] >...	147	3e-35	<input checked="" type="checkbox"/>
gi 22749039 ref NP_689708.1	hypothetical protein FLJ38993 ...	144	2e-34	<input checked="" type="checkbox"/>
gi 13386310 ref NP_082684.1	RIKEN cDNA 2900075G08 [Mus mus...	139	9e-33	<input checked="" type="checkbox"/>
gi 1705957 sp P52159 CNI_DROVI	CORNICHON PROTEIN	139	1e-32	
gi 31238175 ref XP_319722.1	ENSANGP00000019460 [Anopheles ...	138	1e-32	
gi 28207917 emb CAD62612.1	unnamed protein product [Homo s...	129	6e-30	
gi 17564146 ref NP_506278.1	Cornichon protein (16.8 kD) [C...	122	1e-27	<input checked="" type="checkbox"/>
gi 25336821 pir A89261	protein T09E8.3 [imported] - Caenor...	115	9e-26	
gi 20853677 ref XP_136930.1	similar to cornichon homolog [...	79	8e-15	<input checked="" type="checkbox"/>
gi 27679416 ref XP_213960.1	similar to RIKEN cDNA D530030D...	55	2e-07	<input checked="" type="checkbox"/>
gi 7661824 ref NP_054903.1	HSPC163 protein [Homo sapiens] ...	54	3e-07	<input checked="" type="checkbox"/>
gi 8778623 gb AAF79631.1 AC025416_5	F5011.7 [Arabidopsis th...	53	6e-07	
gi 20832303 ref XP_129629.1	expressed sequence AI647760 [M...	53	1e-06	<input checked="" type="checkbox"/>
gi 6321384 ref NP_011461.1	ER-derived vesicles; Erv14p [Sa...	49	1e-05	
gi 18391380 ref NP_563903.1	hypothetical protein [Arabidop...	49	2e-05	
gi 9294117 dbj BAB01968.1	gene_id:T23B7.14~pir T06616~sim...	48	3e-05	
gi 6319687 ref NP_009769.1	Putative ER vesicle protein wit...	47	4e-05	
gi 19115420 ref NP_594508.1	putative er-derived vesicles p...	47	4e-05	
gi 15230426 ref NP_187825.1	expressed protein [Arabidopsis...	46	1e-04	
gi 30682747 ref NP_172701.2	expressed protein [Arabidopsis...	45	2e-04	
gi 13812029 ref NP_113186.1	hypothetical protein [Guillard...	44	4e-04	
gi 15221614 ref NP_176476.1	expressed protein [Arabidopsis...	44	4e-04	
gi 28920672 gb EAA30033.1	hypothetical protein [Neurospora...	44	4e-04	
gi 25336823 pir D96653	hypothetical protein F16P17.3 [impo...	44	4e-04	
gi 31238868 ref XP_319866.1	ENSANGP00000010644 [Anopheles ...	44	5e-04	
gi 15234412 ref NP_192946.1	hypothetical protein [Arabidop...	43	8e-04	
gi 12053355 emb CAB66864.1	hypothetical protein [Homo sapi...	41	0.003	<input checked="" type="checkbox"/>
gi 19115569 ref NP_594657.1	putative er-derived vesicles p...	40	0.007	
gi 24581337 ref NP_608745.1	CG17262-PA [Drosophila melanog...	36	0.082	<input checked="" type="checkbox"/>
gi 8778625 gb AAF79633.1 AC025416_7	F5011.11 [Arabidopsis t...	36	0.095	
gi 17570449 ref NP_508859.1	Predicted CDS, cornichon prote...	36	0.11	<input checked="" type="checkbox"/>

Alignments

☒ >gi|5031639|ref|NP_005767.1| ☒ cornichon-like [Homo sapiens]
☒ gi|27674789|ref|XP_214153.1| ☒ similar to cornichon-like [Homo sapiens] [Rattus n
☒ gi|6225176|sp|O95406|CNIH_HUMAN ☒ Cornichon homolog (TGAM77)
☒ gi|4063709|gb|AAC98388.1| ☒ cornichon [Homo sapiens]
☒ gi|4454684|gb|AAD20960.1| ☒ cornichon protein [Homo sapiens]




gi|12832170|dbj|BAB21993.1|  unnamed protein product [Mus musculus]
gi|12847169|dbj|BAB27463.1|  unnamed protein product [Mus musculus]
gi|22028300|gb|AAH34868.1|  cornichon homolog [Mus musculus]
 Length = 144

Score = 205 bits (521), Expect = 1e-52
 Identities = 116/144 (80%), Positives = 116/144 (80%)

Query: 1 MAFTFAAFCYMXXXXXXXXXXXXXXXXXXWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
 MAFTFAAFCYM WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA
 Sbjct: 1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

 Query: 61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYVQKEGW 120
 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAY QKEGW
 Sbjct: 61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

 Query: 121 CKXXXXXXXXXXXXXXXXXGMIYVLVSS 144
 CK GMIYVLVSS
 Sbjct: 121 CKLAFYLLAFFYYLYGMIYVLVSS 144

>gi|27545445|ref|NP_034049.1|  cornichon homolog [Mus musculus]
gi|6225177|sp|O35372|CNIH_MOUSE  CORNICHON HOMOLOG
gi|2460430|gb|AAC15828.1|  cornichon [Mus musculus]
 Length = 144

Score = 202 bits (515), Expect = 6e-52
 Identities = 115/144 (79%), Positives = 115/144 (79%)

Query: 1 MAFTFAAFCYMXXXXXXXXXXXXXXXXXXWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
 MAFTFAAFCYM WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA
 Sbjct: 1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

 Query: 61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYVQKEGW 120
 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMS PGLYDPTTIMNADILAY QKEGW
 Sbjct: 61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSAPGLYDPTTIMNADILAYCQKEGW 120

 Query: 121 CKXXXXXXXXXXXXXXXXXGMIYVLVSS 144
 CK GMIYVLVSS
 Sbjct: 121 CKLAFYLLAFFYYLYGMIYVLVSS 144

>gi|4894209|gb|AAD32301.1| cornichon-like protein [Homo sapiens]
 Length = 134

Score = 191 bits (485), Expect = 2e-48
 Identities = 105/119 (88%), Positives = 105/119 (88%)

Query: 26 WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYH 85
 WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYH
 Sbjct: 16 WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYH 75

 Query: 86 IWRYMSRPVMSGPGLYDPTTIMNADILAYVQKEGWCKXXXXXXXXXXXXXXXXXGMIYVLVSS 144
 IWRYMSRPVMSGPGLYDPTTIMNADILAY QKEGWCK GMIYVLVSS
 Sbjct: 76 IWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFYLLAFFYYLYGMIYVLVSS 134

>gi|13195570|gb|AAK15762.1|AF329820_1 cornichon [Boltania villosa]
Length = 144

Score = 164 bits (415), Expect = 2e-40
Identities = 87/143 (60%), Positives = 101/143 (70%)

Query: 1 MAFTFAAFCYXXXXXXXXXXXXXXXXXWHIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
MAFTFAAFCY+ W IIAFDELKTDYKNPIDQCN+LNPLVLPEY IH
Sbjct: 1 MAFTFAAFCYIAAIIILTAFLIFFAIWQIIAFDELKTDYKNPIDQCNSLNPLVLPEYAIHI 60

Query: 61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYVQKEGW 120
FF ++FL EW+T+ LNMPL+ Y++WRY+ RPYMS PGLYDPTT+MNAD+L Y +EGW
Sbjct: 61 FFTLLFLWGGWVTVALNMPLIGYNVWRYLHRPVMSAPGLYDPTTVMNADVLTYCMREGW 120

Query: 121 CKXXXXXXXXXXXXXXXXXGMIYVLVS 143
CK MIYVLV+
Sbjct: 121 CKLAFYLISFFYYLYRMIYVLVT 143

>gi|17137046|ref|NP_477068.1| cornichon CG5855-PB [Drosophila melanogaster]
gi|24584585|ref|NP_723959.1| cornichon CG5855-PA [Drosophila melanogaster]
gi|1705956|sp|P49858|CNI_DROME Cornichon protein
gi|1079061|pir|A56724 cni protein - fruit fly (Drosophila melanogaster)
gi|886769|gb|AAA86527.1| cni gene product
gi|7287965|gb|AAF45003.1|AE003406.208 symbol=cni; synonym=BG:DS02740.13; match=score:'1000.0', desc:'GenBank::U28069:cni FBgn0000339 SWISS-PROT:P49858 U28069:93..527', species:'Drosophila melanogaster'; match=method:'sim4', score:'1000.0', desc:'GenBank::U28069:Drosophila melanogaster cornichon (cni) mRNA, complete cds. CDS:93..527; PID:g886769.', species:'Drosophila melanogaster'; match=method:'BLASTX', version:'2.0a19MP-WashU [05-Feb-1998] [Build sol2.5-ultra 01:47:30 05-Feb-1998]', score:'264.0', desc:'>
gi|7298291|gb|AAF53521.1| CG5855-PA [Drosophila melanogaster]
gi|7298292|gb|AAF53522.1| CG5855-PB [Drosophila melanogaster]
Length = 144

Score = 151 bits (381), Expect = 2e-36
Identities = 78/144 (54%), Positives = 96/144 (66%)

Query: 1 MAFTFAAFCYXXXXXXXXXXXXXXXXXWHIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
MAF F AF Y+ +H+IAFDELKTDYKNPIDQCN+LNPLVLPEYL+H
Sbjct: 1 MAFNFTAFTYIIVALIGDAFLIFFAIFHVIAFDELKTDYKNPIDQCNSLNPLVLPEYLLHI 60

Query: 61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYVQKEGW 120
F ++FL EW +L +N+PL+AYHIWRY +RPVMSGPGLYDPTT++ D L +EGW
Sbjct: 61 FLNLLFLFCGEWFSLCINIPLIAYHIWRYKNRPVMSGPGLYDPTTVLKTDTLYRNMREGW 120

Query: 121 CKXXXXXXXXXXXXXXXXXGMIYVLVS 144
K GM+Y L+S+
Sbjct: 121 IKLAVYLISFFYYIYGMVYSLIST 144

☐ >gi|6753470|ref|NP_034050.1| ☒ cornichon-like [Mus musculus]
 gi|22062540|ref|XP_170654.1| ☒ similar to cornichon-like protein [Homo sapiens]
 gi|6225178|sp|O35089|CNIL_MOUSE ☒ CORNICHON-LIKE PROTEIN
 gi|4521254|dbj|BAA21746.2| ☒ cornichon-like protein [Mus musculus]
 gi|28838013|gb|AAH47953.1| Unknown (protein for MGC:50896) [Homo sapiens]
 Length = 160

Score = 147 bits (371), Expect = 3e-35
 Identities = 83/159 (52%), Positives = 93/159 (58%), Gaps = 16/159 (10%)

Query: 1 MAFTFAAFCYMXXXXXXXXXXXXXXXXXXWHIIAFDELKTDYKNPIDQ----- 44
 MAFTFAAFCYM WHIIAFDEL+TD+KNPIDQ
 Sbjct: 1 MAFTFAAFCYMLTLVLCASLIFFVIWHIIAFDELRTDFKNPIDQGNPARARERLKNIERI 60
 Query: 45 CNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPT 104
 C L LV+PEY IH FC+MFLCAAEW+TLGLN+PLL YH+WRY RP +YD
 Sbjct: 61 CCLLRKLVVPEYSIHGLFCLMFLCAAEWVTLGLNIPLLFYHLWRYFHRPADGSEVMYDAV 120
 Query: 105 TIMNADILAYVQKEGWCKXXXXXXXXXXXXXXXXXGMIYVLVS 143
 +IMNADIL Y QKE WCK M+Y LVS
 Sbjct: 121 SIMNADILNYCQKESWCKLAFYLLSFFYYLYSMVYTLVS 159

☐ >gi|22749039|ref|NP_689708.1| ☒ hypothetical protein FLJ38993 [Homo sapiens]
 gi|27805431|sp|Q8TBE1|CNIL_HUMAN ☒ Cornichon-like protein
 gi|18490801|gb|AAH22780.1| ☒ Similar to RIKEN cDNA 2900075G08 gene [Homo sapiens]
 gi|21755779|dbj|BAC04760.1| ☒ unnamed protein product [Homo sapiens]
 gi|26329545|dbj|BAC28511.1| ☒ unnamed protein product [Mus musculus]
 Length = 160

Score = 144 bits (364), Expect = 2e-34
 Identities = 85/160 (53%), Positives = 93/160 (58%), Gaps = 16/160 (10%)

Query: 1 MAFTFAAFCYMXXXXXXXXXXXXXXXXXXWHIIAFDELKTDYKNPIDQCN----- 47
 MAFTFAAFCYM WHIIAFDEL+TD+K+PIDQCN
 Sbjct: 1 MAFTFAAFCYMLSLVLCALIFFAIWHIIAFDELRTDFKSPIDQCNPVHARERLRNIERI 60
 Query: 48 ---LNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPT 104
 L LVLPEY IH+ FC+MFLCA EWLTLGLN+PLL YH WRY P S YDP
 Sbjct: 61 CFLLRKLVLPEYSIHSLFCIMFLCAQEWLTLGLNVPLLFYHFWRYFHCPADSSELAYDPP 120
 Query: 105 TIMNADILAYVQKEGWCKXXXXXXXXXXXXXXXXXGMIYVLVSS 144
 +MNAD L+Y QKE WCK MIY LVSS
 Sbjct: 121 VVMNADTLSYCQKEAWCKLAFYLLSFFYYLYCMIYTLVSS 160

☐ >gi|13386310|ref|NP_082684.1| ☒ RIKEN cDNA 2900075G08 [Mus musculus]
 gi|12851288|dbj|BAB28996.1| ☒ unnamed protein product [Mus musculus]
 Length = 179

Score = 139 bits (349), Expect = 9e-33
 Identities = 84/179 (46%), Positives = 94/179 (52%), Gaps = 35/179 (19%)

Query: 1 MAFTFAAFCYMXXXXXXXXXXXXXXXXXXWHIIAFDELKTDYKNPIDQCN----- 50

Sbjct: 1 MAFTFAAFCYM WHIIAFDEL+TD+K+PIDQCN ++
 Query: 51 -----LVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYH 85
 LVLPEY IH+ FC+MFLCA EWLTLGLN+PLL YH
 Sbjct: 61 CFLLRKVRGVPPGRRKGRRERGGQLVLEYSIHSFLCIMFLCAQEWLTLGLNVPLLFYH 120
 Query: 86 IWRYMSRPVMSGPLYDPTTIMNADILAYVQKEGWCKXXXXXXXXXXXXXGMIYVLVSS 144
 WRY P S YDP +MNAD L+Y QKE WCK MIY LVSS
 Sbjct: 121 FWRYFHCPADSSSELAYDPPVVMNADTSLCYQKEAWCKLAFYLLSFFYYLYCMIYTLVSS 179

>gi|1705957|sp|P52159|CNI_DROVI CORNICHON PROTEIN
 Length = 144

Score = 139 bits (349), Expect = 1e-32
 Identities = 78/144 (54%), Positives = 96/144 (66%)

Query: 1 MAFTFAAFCYMXXXXXXXXXXXXXXWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
 MAF F AF Y+ +H+IAFDELKTDYKNPIDQCN+LNPLVLPEYL+H
 Sbjct: 1 MAFNFTAFTYIIVALIGDAFLIFFAIFHVIAFDELKTDYKNPIDQCNSLNPLVLPEYLLHL 60
 Query: 61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPLYDPTTIMNADILAYVQKEGW 120
 F ++FL EW +L LN+PL+AYHIWRY +RP+MSGPLYDPTT++ D L +EGW
 Sbjct: 61 FLNLLFLFCGEWYSLCLNIPLIAYHIWRYKNRPLMSGPLYDPTTVLKTDTLFRNLREGW 120
 Query: 121 CKXXXXXXXXXXXXXGMIYVLVSS 144
 K GM+Y L+S+
 Sbjct: 121 IKLAVYLISFFYYIYGMVYSLIST 144

>gi|31238175|ref|XP_319722.1| ENSANGP00000019460 [Anopheles gambiae]
 gi|30174276|gb|EAA14788.2| ENSANGP00000019460 [Anopheles gambiae str. PEST]
 Length = 127

Score = 138 bits (348), Expect = 1e-32
 Identities = 68/97 (70%), Positives = 82/97 (84%)

Query: 26 WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYH 85
 +H+IAFDELKTDYKNPIDQCN+LNPLVLPEY +H F ++FL + EWL+L LN+PL+AYH
 Sbjct: 18 FHVIAFDELKTDYKNPIDQCNSLNPLVLPEYGLHILFNLLFLFSGEWLSLALNIPLIAYH 77
 Query: 86 IWRYMSRPVMSGPLYDPTTIMNADILAYVQKEGWCK 122
 IWRY +RPVMS PGLYDPT+IMN D+L +EGW K
 Sbjct: 78 IWRYANRPVMSQPLYDPTSIMNTDVLRACLREGWIK 114

>gi|28207917|emb|CAD62612.1| unnamed protein product [Homo sapiens]
 Length = 94

Score = 129 bits (325), Expect = 6e-30
 Identities = 71/85 (83%), Positives = 71/85 (83%)

Query: 3 FTFAAFCYMXXXXXXXXXXXXXXWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF 62
 FTFAAFCYM WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF
 Sbjct: 1 FTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF 60

Query: 63 CVMFLCAAEWLTLGLNMPLLAYHIW 87
 CVMFLCAAEWLTLGLNMPLLAYHIW
 Sbjct: 61 CVMFLCAAEWLTLGLNMPLLAYHIW 85

>gi|17564146|ref|NP_506278.1| Cornichon protein (16.8 kD) [Caenorhabditis elegans]
 gi|20141964|sp|Q22361|YFR3_CAEEL Hypothetical 16.8 kDa protein T09E8.3 in chromos
 gi|7507545|pir|T24750 hypothetical protein T09E8.3 - Caenorhabditis elegans
 gi|5824608|emb|CAB01516.2| Hypothetical protein T09E8.3 [Caenorhabditis elegans]
 Length = 145

Score = 122 bits (305), Expect = 1e-27
 Identities = 66/144 (45%), Positives = 87/144 (60%)

Query: 1 MAFTFAAFCYMXXXXXXXXXXXXXWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
 MAFTFAAFCY+ + +I DEL+TDYKNPI+QC LN L+LPEY+IH
 Sbjct: 1 MAFTFAAFCYLLALIAVGFCIFFAIYTVICVDELRTDYKNPIEQCRNLNQLILPEYIIHG 60
 Query: 61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYVQKEGW 120
 F V+F+ + + +++ N+PL YHI+ Y RPVMSGPG+YDPTTI+N L+ + W
 Sbjct: 61 TFTVLFIFSWQLISILANLPLAFYHIYTYAKRPVMSGPGIYDPTTILNRSTLSSTLRISW 120
 Query: 121 CKXXXXXXXXXXXXGMIYVLVSS 144
 K MIY LV+S
 Sbjct: 121 IKLAFYLVSFYLYAMIYTLVTS 144

>gi|25336821|pir|A89261 protein T09E8.3 [imported] - Caenorhabditis elegans
 Length = 136

Score = 115 bits (289), Expect = 9e-26
 Identities = 60/122 (49%), Positives = 80/122 (65%)

Query: 1 MAFTFAAFCYMXXXXXXXXXXXXXWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
 MAFTFAAFCY+ + +I DEL+TDYKNPI+QC LN L+LPEY+IH
 Sbjct: 1 MAFTFAAFCYLLALIAVGFCIFFAIYTVICVDELRTDYKNPIEQCRNLNQLILPEYIIHG 60
 Query: 61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYVQKEGW 120
 F V+F+ + + +++ N+PL YHI+ Y RPVMSGPG+YDPTTI+N L+ + W
 Sbjct: 61 TFTVLFIFSWQLISILANLPLAFYHIYTYAKRPVMSGPGIYDPTTILNRSTLSSTLRISW 120
 Query: 121 CK 122
 K
 Sbjct: 121 IK 122

>gi|20853677|ref|XP_136930.1| similar to cornichon homolog [Mus musculus]
 Length = 246

Score = 79.3 bits (194), Expect = 8e-15
 Identities = 39/80 (48%), Positives = 44/80 (55%), Gaps = 19/80 (23%)

Query: 7 AFCYMXXXXXXXXXXXXXWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMF 66
 AFCYM WHI+AF+E+K DYK+PIDQC+TLNP
 Sbjct: 186 AFCYMLALLLITVLSFFIIWHILAFNEMKNDYKSPIDQCDTLNP----- 229

Query: 67 LCAAEWLTLGLNMPLLAYHI 86
 EWLTLGLNMP LAYHI
 Sbjct: 230 ---PEWLTGLGLNMPPLAYHI 246

>gi|27679416|ref|XP_213960.1| similar to RIKEN cDNA D530030D03 [Mus musculus]
 Length = 139

Score = 55.1 bits (131), Expect = 2e-07
 Identities = 36/118 (30%), Positives = 56/118 (47%), Gaps = 1/118 (0%)

Query: 26 WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYH 85
 + II +L+ DY N C+ LN V+PE + H F V+ L + W+ LN+P+ ++
 Sbjct: 22 YFIITLSDLECDYINARSCCSKLNKWWIPELVGHTFVTVLMLVSLHWWIFLLNLPVATWN 81
 Query: 86 IWRYMSRPVMSGPGLYDPTTIMNADILAYVQKEGWCKXXXXXXXXXXXXXGMIYVLVS 143
 I+R++ P G++DPT I N L KE K MI L++
 Sbjct: 82 IYRFIMVP-SGNMGVFDPTTEIHNRRQLKSHMKEAMIKLGFYLLCFFMYLYSMILALIN 138

>gi|7661824|ref|NP_054903.1| HSPC163 protein [Homo sapiens]
 gi|12229837|sp|Q9P003|H163_HUMAN Protein HSPC163
 gi|6841548|gb|AAF29127.1|AF161512_1 HSPC163 [Homo sapiens]
 gi|12653595|gb|AAH00573.1|AAH00573 HSPC163 protein [Homo sapiens]
 Length = 139

Score = 54.3 bits (129), Expect = 3e-07
 Identities = 36/118 (30%), Positives = 54/118 (45%), Gaps = 1/118 (0%)

Query: 26 WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYH 85
 + II +L+ DY N C+ LN V+PE + H V+ L + W LN+P+ ++
 Sbjct: 22 YFIITLSDLECDYINARSCCSKLNKWWIPELIGHTIVTVLLLSLHWFIFLLNLPVATWN 81
 Query: 86 IWRYMSRPVMSGPGLYDPTTIMNADILAYVQKEGWCKXXXXXXXXXXXXXGMIYVLVS 143
 I+RY+ P G++DPT I N L KE K MI L++
 Sbjct: 82 IYRYIMVP-SGNMGVFDPTTEIHNRRQLKSHMKEAMIKLGFHLLCFFMYLYSMILALIN 138

>gi|8778623|gb|AAF79631.1|AC025416_5 F5011.7 [Arabidopsis thaliana]
 Length = 455

Score = 53.1 bits (126), Expect = 6e-07
 Identities = 27/83 (32%), Positives = 41/83 (49%), Gaps = 5/83 (6%)

Query: 26 WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYH 85
 +H++ +L+ DY NP D + +N +VLPE+++ CV +L W L +P L Y+
 Sbjct: 15 PHLVCLADLEFDYINPYDSASRINSVVLPEFIVQGVLCVFYLLTGHWFMTLLCLPYLYYN 74
 Query: 86 IWRYMSRPVMSGPGLYDPTTIMN 108
 Y R L D T I N
 Sbjct: 75 FHLYSKR-----QHLVDVTEIFN 92

>gi|20832303|ref|XP_129629.1| expressed sequence AI647760 [Mus musculus]
 gi|12862150|dbj|BAB32366.1| unnamed protein product [Mus musculus]
 Length = 139

Score = 52.8 bits (125), Expect = 1e-06
 Identities = 35/118 (29%), Positives = 54/118 (45%), Gaps = 1/118 (0%)

Query: 26 WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYH 85
 + II +L+ DY N C+ LN V+PE + H V+ L + W LN+P+ ++
 Sbjct: 22 YFIITLSDLECDYINARSCSKLNKWIPELVGHTIVTVLMLVSLHWFIFLLNLPVATWN 81

Query: 86 IWRYSRPMVSGPGLYDPTTIMNADILAYVQKEGWCKXXXXXXXXXXXXXGMIYVLVS 143
 I+R++ P G++DPT I N L KE K MI L++
 Sbjct: 82 IYRFIMVP-SGNMGVFDPTTEIHNRGQLKSHMKEAMIKLGFYLLCFFMYLYSMILALIN 138

>gi|6321384|ref|NP_011461.1| ER-derived vesicles; Erv14p [Saccharomyces cerevisiae]
 gi|1723832|sp|P53173|ERV4_YEAST ER-DERIVED VESICLES PROTEIN ERV14
 gi|2132531|pir|S64058 probable membrane protein YGL054c - yeast (Saccharomyces cerevisiae)
 gi|1322550|emb|CAA96756.1| ORF YGL054c [Saccharomyces cerevisiae]
 Length = 138

Score = 49.3 bits (116), Expect = 1e-05
 Identities = 22/58 (37%), Positives = 36/58 (62%)

Query: 29 IAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYHI 86
 I + +L+ DY NPI+ C+ +N L+ PE +H ++FL W LN+P+LAY++
 Sbjct: 25 ILYADLEADYINPIELCSKVNLITPEAALHGALSLLFLLNGYWFVFLNLPVLAYNL 82

>gi|18391380|ref|NP_563903.1| hypothetical protein [Arabidopsis thaliana]
 Length = 118

Score = 48.5 bits (114), Expect = 2e-05
 Identities = 22/67 (32%), Positives = 36/67 (53%)

Query: 26 WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYH 85
 +H++ +L+ DY NP D + +N +VLPE+++ CV +L W L +P L Y+
 Sbjct: 15 FHLVCLADLEFDYINPYDSASRINSVVLPEFIVQGVLCVFYLLTGHWFMTLLCLPYLYYN 74

Query: 86 IWRYSR 92
 Y R
 Sbjct: 75 FHLYSKR 81

>gi|9294117|dbj|BAB01968.1| gene_id:T23B7.14~pir|T06616~similar to unknown prot
 [Arabidopsis thaliana]
 Length = 166

Score = 47.8 bits (112), Expect = 3e-05
 Identities = 20/67 (29%), Positives = 36/67 (53%)

Query: 26 WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYH 85
 + +I +L+ DY NP + +N LV+PE+++ C++FL W+ + +P+ YH

Sbjct: 24 YQVICLTDL EADYLNPFETSTRINRLVIPEFILQGS LCLLFLLTWHWVFFLVAVPVTVYH 83

Query: 86 IWRYSR 92

Y R

Sbjct: 84 AMLYKER 90

>gi|6319687|ref|NP_009769.1| Putative ER vesicle protein with similarity to Erv1
[Saccharomyces cerevisiae]
gi|586332|sp|P38312|YB60_YEAST Hypothetical 16.3 kDa protein in DUR1,2-AME1 inter
gi|626236|pir|S46084 probable membrane protein YBR210w - yeast (Saccharomyces
cerevisiae)
gi|536592|emb|CAA85174.1| ORF YBR210w [Saccharomyces cerevisiae]
Length = 142

Score = 47.4 bits (111), Expect = 4e-05
Identities = 22/57 (38%), Positives = 34/57 (59%)

Query: 29 IAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYH 85
I + +L+ DY N I+ C +N L +PE ++ AF +FL W LN+P+LAY+
Sbjct: 28 ILYGDLEADYINSIELCKRVNRLSVPEAILQAFISALFLFNGYWFVFLNVPVLAYN 84

>gi|19115420|ref|NP_594508.1| putative er-derived vesicles protein [Schizosaccha
gi|6226447|sp|O14038|YEY5_SCHPO Hypothetical protein C2C4.05 in chromosome I
gi|7490394|pir|T38516 cornichon homolog - fission yeast (Schizosaccharomyces pom
gi|2414616|emb|CAB16365.1| putative er-derived vesicles protein [Schizosaccharomy
Length = 134

Score = 47.4 bits (111), Expect = 4e-05
Identities = 31/101 (30%), Positives = 51/101 (50%), Gaps = 5/101 (4%)

Query: 6 AAF CYMXXXXXXXXXXXXXXXXWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVM 65
+A+ Y + + + +LK D+ NPID LN VLPE AF ++
Sbjct: 3 SAWIYFTSLMLTCANIMLQMYFTVMYSDLKDDFINPIDLSRKLNWYVLPPEMGFQAFSALL 62
Query: 66 FLCAAEWLTLGLNMPLLAYHIWRYSRPMMSGPGLYDPTTI 106
L + W+T LN+P+LA++ ++ +MS ++D TTI
Sbjct: 63 LLLSGAWITFLLNVPMLAWN-----AKMIMSNTHMHDSTTI 98

>gi|15230426|ref|NP_187825.1| expressed protein [Arabidopsis thaliana]
gi|12322050|gb|AAG51073.1|AC069472_13 unknown protein; 8145-9251 [Arabidopsis tha
gi|30017219|gb|AAP12843.1| At3g12180 [Arabidopsis thaliana]
Length = 146

Score = 45.8 bits (107), Expect = 1e-04
Identities = 20/67 (29%), Positives = 36/67 (53%)

Query: 26 WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYH 85
+ +I +L+ DY NP + +N LV+PE+++ C++FL W+ + +P+ YH
Sbjct: 24 YQVICLTDL EADYLNPFETSTRINRLVIPEFILQGS LCLLFLLTWHWVFFLVAVPVTVYH 83

Query: 86 IWRYSR 92
Y R
Sbjct: 84 AMLYKER 90

>gi|30682747|ref|NP_172701.2| expressed protein [Arabidopsis thaliana]
 gi|28416577|gb|AAO42819.1| At1g12390 [Arabidopsis thaliana]
 Length = 137

Score = 45.1 bits (105), Expect = 2e-04
 Identities = 21/67 (31%), Positives = 35/67 (52%)

Query: 26 WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYH 85
 + ++ +L+ DY NP D + +N +VLPE+++ CV +L W L +P L Y+
 Sbjct: 23 YQLVCLADLEFDYINPYDSASRINSVVLPEFIVQGVLCVFYLLTGHWFMTLLCLPYLYYN 82

Query: 86 IWRYMSR 92

Y R

Sbjct: 83 FHLYSKR 89

>gi|13812029|ref|NP_113186.1| hypothetical protein [Guillardia theta]
 gi|13812086|ref|NP_113160.1| hypothetical protein [Guillardia theta]
 gi|13812215|ref|NP_113346.1| hypothetical protein [Guillardia theta]
 gi|25396794|pir|G90096 hypothetical protein orf160 [imported] - Guillardia theta
 nucleomorph
 gi|25396978|pir|H90129 hypothetical protein orf160 [imported] - Guillardia theta
 nucleomorph
 gi|25397012|pir|B90133 hypothetical protein orf160 [imported] - Guillardia theta
 nucleomorph
 gi|13794354|gb|AAK39731.1|AF083031_88 hypothetical protein [Guillardia theta]
 gi|13794404|gb|AAK39781.1|AF083031_145 hypothetical protein [Guillardia theta]
 gi|13794527|gb|AAK39902.1|AF165818_110 hypothetical protein [Guillardia theta]
 Length = 160

Score = 44.3 bits (103), Expect = 4e-04
 Identities = 20/53 (37%), Positives = 31/53 (58%)

Query: 33 ELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYH 85
 +L TD NP++ C+ +N L +PEYL H F + F+ W+ LN P + Y+
 Sbjct: 38 DLSTDVTNPNVEVCDKVNQLKVPEYLAHLFLSIAFVIRGWWIVGFLNFPFIFYN 90

>gi|15221614|ref|NP_176476.1| expressed protein [Arabidopsis thaliana]
 gi|26452314|dbj|BAC43243.1| unknown protein [Arabidopsis thaliana]
 gi|28416891|gb|AAO42976.1| At1g62880 [Arabidopsis thaliana]
 Length = 137

Score = 44.3 bits (103), Expect = 4e-04
 Identities = 22/64 (34%), Positives = 35/64 (54%)

Query: 26 WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYH 85
 + +I+ +L+ DY NP D + +N +VLPE ++ F CV +L W L +P L Y+
 Sbjct: 23 YQLISLADLEFDYINPYDSASRINFVVLPEVILQGFVLCVFLVTGHWFMTLLCLPYLYYN 82

Query: 86 IWRY 89

Y

Sbjct: 83 FHLY 86

☐ >gi|28920672|gb|EAA30033.1| hypothetical protein [Neurospora crassa]
Length = 138

Score = 43.9 bits (102), Expect = 4e-04
Identities = 38/114 (33%), Positives = 55/114 (48%), Gaps = 7/114 (6%)

Query: 29 IAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTGLNMPLLAYHIWR 88
I + +L+ DY NPID CN LN ++PE +H F +FL WL L LN+PLLA+++
Sbjct: 27 IMYSDLECDYINPIDLCNRLNTYIIEVAVHGFLTFLFLINGYWLPLVLNLPLLAWN-- 84

Query: 89 YMSRPVMSGPGLYDPTTIMNADILAYVQKEGWCKXXXXXXXXXXXXXGMIYVLV 142
+ ++ L D T I L +KE + K MI L+
Sbjct: 85 ---KKIVDNAHLDATEIFRK--LNVHKKESFTKLGFHLILFFFYLYSMIVALI 133

☐ >gi|25336823|pir|D96653 hypothetical protein F16P17.3 [imported] - Arabidopsis
gi|8493595|gb|AAF75818.1|AC011000.21 Contains similarity to a 14kDa protein found
vesicles from Saccharomyces cerevisiae gi|6321384.
ESTs gb|T22150, gb|AI100633, gb|AA395672 come from this
gene. [Arabidopsis thaliana]
Length = 126

Score = 43.9 bits (102), Expect = 4e-04
Identities = 22/64 (34%), Positives = 35/64 (54%)

Query: 26 WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTGLNMPLLAYH 85
+ +I+ +L+ DY NP D + +N +VLPE ++ F CV +L W L +P L Y+
Sbjct: 23 YQLISLADLEFDYINPYDSASRINFVVLPELILQGLCVFYLVTHGHWFALLCVPYLYYN 82

Query: 86 IWRY 89
Y
Sbjct: 83 FHLV 86

☐ >gi|31238868|ref|XP_319866.1| ENSANGP00000010644 [Anopheles gambiae]
gi|21302562|gb|EAA14707.1| ENSANGP00000010644 [Anopheles gambiae str. PEST]
Length = 165

Score = 43.5 bits (101), Expect = 5e-04
Identities = 23/83 (27%), Positives = 42/83 (50%), Gaps = 1/83 (1%)

Query: 26 WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTGLNMPLLAYH 85
+++I +L+ DY N + C+ LN +P+ HAF + L W+ +N+P++ +
Sbjct: 33 YYLIILSDLECDYLNAQECCSKLNFWSIPKLAHAFLTFVLLIHGHWMLCLVNLPMVGWL 92

Query: 86 IWRYMSRPVMSGPGLYDPTTIMN 108
++ P G+YDP I N
Sbjct: 93 VYEQYRVPA-GNIGIYDPAEIH 114

☐ >gi|15234412|ref|NP_192946.1| hypothetical protein [Arabidopsis thaliana]
gi|7485571|pir|T06616 hypothetical protein F16J13.160 - Arabidopsis thaliana
gi|4586114|emb|CAB40950.1| putative protein [Arabidopsis thaliana]
gi|7267910|emb|CAB78252.1| putative protein [Arabidopsis thaliana]

Length = 145

Score = 42.7 bits (99), Expect = 8e-04
Identities = 20/60 (33%), Positives = 33/60 (55%)

Query: 33 ELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSR 92
+L+ D NP D + +N +VLPE+ + C+ ++ W L++P L Y+I YM R
Sbjct: 40 DLEFDRINPYDVSSRINRMVLPEFGLQGLLCLYYILTGHWFMAVLSLPHLFYNIRLYMKR 99

☐ >gi|12053355|emb|CAB66864.1| ☒ hypothetical protein [Homo sapiens]
Length = 92

Score = 40.8 bits (94), Expect = 0.003
Identities = 21/63 (33%), Positives = 34/63 (53%)

Query: 26 WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYH 85
+ II +L+ DY N C+ LN V+PE + H V+ L + W LN+P+ ++
Sbjct: 22 YFIITLSDLCDYINARSCSKLNKWIPELIGHTIVTVLLLSLHWFIFLLNLPVATWN 81

Query: 86 IWR 88
I+R
Sbjct: 82 IYR 84

☐ >gi|19115569|ref|NP_594657.1| putative er-derived vesicles protein similar to ye
[Schizosaccharomyces pombe]
☐ gi|7768496|emb|CAB90792.1| putative er-derived vesicles protein similar to yeast
[Schizosaccharomyces pombe]
Length = 141

Score = 39.7 bits (91), Expect = 0.007
Identities = 18/32 (56%), Positives = 23/32 (71%)

Query: 28 IIAFDELKTDYKNPIDQCNTLNPLVLPEYLIH 59
+I F +L+ DY NPID CN LN LV+PE + H
Sbjct: 31 VIMFSDLEMDYINPIDLCNKLNDLVMPETISH 62

☐ >gi|24581337|ref|NP_608745.1| ☒ CG17262-PA [Drosophila melanogaster]
☐ gi|7295853|gb|AAF51153.1| ☒ CG17262-PA [Drosophila melanogaster]
Length = 157

Score = 36.2 bits (82), Expect = 0.082
Identities = 25/87 (28%), Positives = 46/87 (52%), Gaps = 1/87 (1%)

Query: 26 WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYH 85
++++ +L+ DY N + C LN V+P++ HA CV+ L W+ LN+P++ +
Sbjct: 25 YYVLTADLECDYLNAQECCRRNFWVIPKFGSHALLCVLLLLGGHWVMFLLNLPVVIWL 84

Query: 86 IWRYSRPVMSGPLYDPTTIMNADIL 112
+ + R G+YDP I + +L
Sbjct: 85 FYE-LHRQRRDSLGVYDPVDIHSRGLL 110

☐ >gi|8778625|gb|AAF79633.1|AC025416_7 F5011.11 [Arabidopsis thaliana]
Length = 110

Score = 36.2 bits (82), Expect = 0.095
Identities = 14/42 (33%), Positives = 26/42 (61%)

Query: 26 WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFL 67
+ ++ +L+ DY NP D + +N +VLPE+++ CV +L
Sbjct: 23 YQLVCLADLEFDYINPYDSASRINSVVLPEFIVQGVLCVFYL 64

☐ >gi|17570449|ref|NP_508859.1| ☒ Predicted CDS, cornichon protein [Caenorhabditis
gi|13775541|gb|AAK39349.1| Hypothetical protein Y64H9A.1 [Caenorhabditis elegans]
Length = 56

Score = 35.8 bits (81), Expect = 0.11
Identities = 20/51 (39%), Positives = 26/51 (50%)

Query: 94 VMSGPGLYDPTTIMNADILAYVQKEGWCKXXXXXXXXXXXXXGMIYVLVSS 144
+M GPG+YDPTTI+N L+ + W K MIY LV+S
Sbjct: 1 MMPGPGIYDPTTILNRSTLSSTLRISWIKLAFYLVSFYYLYVMIYTLVTS 51

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
Posted date: Jun 6, 2003 1:54 AM
Number of letters in database: 463,592,631
Number of sequences in database: 1,442,039

Lambda	K	H
0.330	0.143	0.492

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 113,816,301

Number of Sequences: 1442039

Number of extensions: 4147288

Number of successful extensions: 8257

Number of sequences better than 10.0: 37

Number of HSP's better than 10.0 without gapping: 37

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 8216

Number of HSP's gapped (non-prelim): 38

length of query: 144

length of database: 463,592,631

effective HSP length: 120

effective length of query: 24

effective length of database: 290,547,951

effective search space: 6973150824

effective search space used: 6973150824

T: 11

A: 40

X1: 15 (7.2 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 40 (21.9 bits)

S2: 65 (29.6 bits)